Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims

1. (Currently amended) A method for analysing a heterogeneous sample of peptides, or protein or peptide fragments, the method comprising:

   (a) separating the heterogeneous sample of peptides, or protein or peptide fragments, into heterogeneous classes by binding members of each class to a spaced apart defined location on an array, wherein more than one peptide, protein or peptide fragment binds to each defined location on the array, and wherein members of each class have a motif common to that class; and

   (b) characterising the peptides, or protein or peptide fragments, in each class by determining the mass of the peptides, or protein or peptide fragments in the heterogenous classes, and determining the abundance of peptides, or protein or peptide fragments, of different mass in the heterogeneous classes.

2. (Currently pending) A method according to Claim 1 wherein the heterogeneous sample of peptides, or protein or peptide fragments, is an extract of the total protein content of a cell or tissue type.

3. (Currently pending) A method according to Claim 1 wherein, prior to performing step (a), the heterogeneous sample of fragments is formed by fragmenting a heterogeneous sample of proteins or peptides.

4. (Currently pending) A method according to Claim 3 wherein the fragmenting is performed by chemical or enzymatic cleavage.

5. (Currently pending) A method according to Claim 3 wherein the fragmenting is performed using a sequence-directed cleavage mechanism.

6. (Currently pending) A method according to Claim 3 wherein the fragmenting is performed by digestion of the heterogeneous sample of proteins or peptides with trypsin.

7. (Currently pending) A method according to claim 1 wherein the motif in each peptide, or protein or peptide fragment, is at the same location in each peptide, or protein or peptide fragment, relative to the C-terminus, the N-terminus, or an internal feature.

8. (Currently pending) A method according to claim 1 wherein the sample is a heterogeneous sample of fragments of proteins or peptides and the motif in each fragment is at the same location in each fragment, relative to the site of cleavage.

9. (Currently pending) A method according to claim 1 wherein the motif in each peptide, or protein or peptide fragment, is three, four, five, six or more amino acids in length.

10. (Currently pending) A method according to claim 1 wherein the motif contains three, four or five variable amino acids, the other amino acids in the motif being constant between all peptides, or protein or peptide fragments.

11. (Currently pending) A method according claim 1 wherein the motif is at the C-terminus.

12. (Withdrawn) A method according to claim 1 wherein the motif is at the N-terminus.

13. (Currently pending) A method according to claim 1 wherein the array comprises a number of different types of binding molecule, each type immobilised at a spaced apart defined location on the array, wherein each type of binding molecule is capable of binding specifically to a motif and wherein different types of binding molecule have different binding specificities.

14. (Currently pending) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture at least 10% of the peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from at least 10% of the proteins or peptides in the unfragmented sample.

15. (Withdrawn) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture at least 50% of the proteins or peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from at least 50% of the proteins or peptides in the unfragmented sample.

16. (Withdrawn) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture substantially 100% of the proteins or peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from substantially 100% of the proteins or peptides in the unfragmented sample.

17. (Currently pending) A method according to claim 13 wherein the array has at least about 10, 50, 100, 150, 200, 250, 300, or more different types of binding molecules provided thereon.

18. (Currently pending) A method according to claim 13 wherein at least one type of the binding molecule is an antibody or a fragment or variant thereof.

19. (Withdrawn) A method according to claim 13 wherein at least one of the types of the binding molecule is an aptamer.

20. (Withdrawn) A method according to claim 13 wherein at least one of the types of the binding molecule is a polynucleotide.

21. (Currently pending) A method according to claim 1 wherein step (b) comprises characterising bound peptides, or protein or peptide fragments, at the defined and discrete locations on the array.

22. (Canceled)

23. (Canceled)

24. (Currently pending) A method according to claim 1 wherein step (b) comprises

characterising the peptides, or protein or peptide fragments, in the heterogeneous classes by desorption mass spectrometry or collision induced dissociation mass spectrometry.

25. (Currently pending) A method according to claim 1 wherein the information derived from step (b) is used to determine the identity of the parent protein or peptide in the unfragmented heterogeneous sample from which a detected protein or peptide fragment is derived.

26. (Currently pending) A method according to claim 1 wherein the information derived from step (b) is used to determine the abundance of the parent protein or peptide in ~~a~~ the unfragmented heterogeneous sample from which the detected protein or peptide fragment is derived.

27. (Currently pending) A method for identifying differences in composition between two or more heterogeneous fragmented or unfragmented samples of peptides, or protein or peptide fragments, comprising analysing each sample by the method according to claim 1 and comparing the results, thereby to identify any differences.

Claims 28-49 (canceled).